

209TFO" SEETSOOT

g914899	GAGE-1	-MSWRGR-STYRPRRRYVEPPEMIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g914901	GAGE-2	-MSWRGR-STYRPRRRYVEPPEMIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g914903	GAGE-3	MNLSRGKSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g914905	GAGE-4	-MSWRGRSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g914907	GAGE-5	-MSWRGRSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g914909	GAGE-6	-MSWRGRSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g3300090	GAGE-7	-MSWRGRSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g3511025	GAGE-7B	-MSWRGRSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
g3511023	GAGE-8	-MSWRGR-STYRPRRRYVEPPEMIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
4030354CB1+2_ORF1		-MSWRGRSTYYWPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
980547.1+2_ORF1		-MSWRGR-STYRPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
064516CB1+2_ORF1		-MTWRGR-STYRPRRRYVQPPVEIGPMRP-EQFSDEVEPATPEEGEPATQRQDPAAAQ
		::: * **: ***::** *::: *::: *::: *::: *::: *::: *::: *::: *::: *::: *
g914899	GAGE-1	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEE-EMRSHY
g914901	GAGE-2	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g914903	GAGE-3	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g914905	GAGE-4	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g914907	GAGE-5	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g914909	GAGE-6	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g3300090	GAGE-7	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g3511025	GAGE-7B	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
g3511023	GAGE-8	GE-DEGASAGQPKPEADSQEQGHPTGTCECEDGPDGQEMDPPNPEEVKTPEEKEKQSQ
4030354CB1+2_ORF1		REDDQAAETQVPDLADLQELCQTKTGCGEGTGVKILPKAEHFKMPEAGEGKSQV
980547.1+2_ORF1		REDDQAAETQVPDLADLQELCQTKTGCGEGTGVKILPKAEHFKMPEAGEGKSQV
064516CB1+2_ORF1		* **::: * **::: * **::: * **::: * **::: * **::: * **::: * **::: * **::: *
g914899	GAGE-1	VAQTGILWLLMNNCFNLNLSRKP

FIGURE 1

2097797.1+1_ORF1

g499122	MAGE-3B	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAAES
g533523	MAGE-6	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAAES
g7280335	MAGE-A3	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAAES
g468826	MAGE-3	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAAES
g7280334	MAGE-A2b	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAADSP
g7280332	MAGE-A2a	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAADSP
g436181	MAGE-2	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAADSP
g7280333	MAGE-A12	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAADSP
g499346	MAGE-12	MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAAASSSS-TLVEVTLGEVPAADSP
g533517	MAGE-4b	MSSEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g499124	MAGE-X2	MSSEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g1125018	MAGE-41	MSSEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g533515	MAGE-4a	MSLEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g1125014	MAGE-4	MSLEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g533513	MAGE-11	MSLEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g533528	MAGE-9	MSLEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
1471808CB1+1_ORF1		MSLEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
1097797.1+1_ORF1		MSLEKQSQHCKPEEGVEAQEEALGLVGAQAPATEEQEAAASSSS-TLVEVTLREVPAAES
g499122	MAGE-3B	DPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g533523	MAGE-6	DPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g7280335	MAGE-A3	DPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g468826	MAGE-3	DPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g7280334	MAGE-A2b	SPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g7280332	MAGE-A2a	SPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g436181	MAGE-2	SPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g7280333	MAGE-A12	SPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g499346	MAGE-12	SPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g533517	MAGE-4b	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g499124	MAGE-X2	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g1125018	MAGE-41	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g533515	MAGE-4a	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g1125014	MAGE-4	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g533513	MAGE-11	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
g533528	MAGE-9	GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
1471808CB1+1_ORF1		GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL
1097797.1+1_ORF1		GPPSPQSGASSLPTTMNYPWMSQSYEDSSNQEEEGPSTFPDL---ESEFQAALSRKVAKL

FIGURE 2A

Inventors: Jones et al.

Title: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS

Serial No.: To Be Assigned

1005180 011600

MAGE-3B	VHFLLLKYRAREPVTKAEMLSVGNWQYFFPVIFSKASDSLQLVFGIELMEVDPIGHVY
MAGE-6	VHFLLLKYRAREPVTKAEMLSVGNWQYFFPVIFSKASDSLQLVFGIELMEVDPIGHVY
MAGE-A3	VHFLLLKYRAREPVTKAEMLSVGNWQYFFPVIFSKASSSLQLVFGIELMEVDPIGHLY
MAGE-3	VHFLLLKYRAREPVTKAEMLSVGNWQYFFPVIFSKASSELQLVFGIELMEVDPIGHLY
MAGE-A2b	VHFLLLKYRAREPVTKAEMLESVLRNCQDFPPVIFSKASSELQLVFGIEVWVPISHLY
MAGE-A2a	VHFLLLKYRAREPVTKAEMLESVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-2	VHFLLLKYRAREPVTKAEMLESVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-A12	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-12	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-4b	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-X2	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-41	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-4a	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-4	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-11	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-9	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
1_1471808CB1+1_ORF1	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
1_1097797.1+1_ORF1	VHFLLLKYRAREPVTKAEMLSVLRNCQDFPPVIFSKASEYLQLVFGIEVWVPISHLY
MAGE-3B	IFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPEEKIWEELSVLVEFEGRED
MAGE-6	IFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPEEKIWEELSVLVEFEGRED
MAGE-A3	IFATCLGLSYDGLLGDNQIMPKAGLLIIIVLAIIAREGDCAPEEKIWEELSVLVEFEGRED
MAGE-3	IFATCLGLSYDGLLGDNQIMPKAGLLIIIVLAIIAREGDCAPEEKIWEELSVLVEFEGRED
MAGE-A2b	ILVTCLGLSYDGLLGDNQIMPKTGLLIIIVLAIIAIEGDCAPEEKIWEELSMLVEFEGRED
MAGE-A2a	ILVTCLGLSYDGLLGDNQIMPKTGLLIIIVLAIIAIEGDCAPEEKIWEELSMLVEFEGRED
MAGE-2	ILVTCLGLSYDGLLGDNQIMPKTGLLIIIVLAIIAIEGDCAPEEKIWEELSMLVEFEGRED
MAGE-A12	ILVTCLGLSYDGLLGDNQIMPKTGLLIIIVLAIIAIEGDCAPEEKIWEELSMLVEFEGRED
MAGE-12	ILVTCLGLSYAGLLGDNQIVPKTGLLIIIVLAIIAKEGDCAPEEKIWEELSVLASDGRD
MAGE-4b	TLVTCLGLSYDGLLGNQIIPKPTGLLIIIVLGTIAMEGDSASEEEIWEELGMGVYDGRH
MAGE-X2	TLVTCLGLSYDGLLGNQIIPKPTGLLIIIVLGTIAMEGDSASEEEIWEELGMGVYDGRH
MAGE-41	TLVTCLGLSYDGLLGNQIIPKPTGLLIIIVLGTIAMEGDSASEEEIWEELGMGVYDGRH
MAGE-4a	TLVTCLGLSYDGLLGNQIIPKPTGLLIIIVLGTIAMEGDSASEEEIWEELGMGVYDGRH
MAGE-4	TLVTCLGLSYDGLLGNQIIPKPTGLLIIIVLGTIAMEGDSASEEEIWEELGMGVYDGRH
MAGE-11	VLVTSNLVSDGIIQCNQSMPSKGLIIIVLGVIFMEGNCIPEEVMWEVLISMGVYAGREH
MAGE-9	ILVTALGLSDCSMLGDGHSMPKAAALLIIIVLGVILTCKNCAPEEVIWEALSVMGVYVKGKH
1_1471808CB1+1_ORF1	IFATCLGLSYDGLLGDNQIMPKTGFLIIILAIIAKEGDCAPEEKIWEELSVLVEFEGRED
1_1097797.1+1_ORF1	ILVTALGLSDCSMLGDGHSMPKAAALLIIIVLGVILTCKNCAPEEVIWEALSVMGVYVKGKH

FIGURE 2B

9499122	MAGE-3B	PRISYPLLHEWALREGEE--
9533523	MAGE-6	PRISYPLLHEWALREGEE--
9728033	MAGE-A3	PHISYPLHEWVLREGEE--
9468826	MAGE-3	PHISYPLHEWVLREGEE--
97280334	MAGE-A2b	PHISYPLLHEWALREGEE--
97280332	MAGE-A2a	PHISYPLLHEWALREGEE--
9436181	MAGE-2	PHISYPLLHEWALREGEE--
97280333	MAGE-A12	PHISYPLLHEWAFREGEE--
9499346	MAGE-12	PHIYPPLHEWAFREGEE--
9533517	MAGE-4b	PHIYPPLHEWAFREGEE--
9499124	MAGE-X2	VRIAYPSLUREAALLLEEFGV
91125018	MAGE-41	VRIAYPSLUREAALLLEEFGV
9533515	MAGE-4a	VRIAYPSLUREAALLLEEFGV
91125014	MAGE-4	VRIAYPSLUREAALLLEEFGV
9533513	MAGE-11	DPTYSPLLYEDALREBQEGV
9533528	MAGE-9	EPICYPSTLYEVLGEEQEGV
1471808CB1+1_ORF1		PRISYPLLHEWALREGEE--
1097797.1+1_ORF1		EPICYPSTLYEVLGEEQEGV

FIGURE 2C